## Alan J Cooper

## List of Publications by Year in descending order

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315

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297 32,379 88
papers citations h-index

315

docs citations

h-index g-index

315
25551
times ranked citing authors

165

#	Article	IF	CITATIONS
1	Massive migration from the steppe was a source for Indo-European languages in Europe. Nature, 2015, 522, 207-211.	27.8	1,435
2	Ancient human genomes suggest three ancestral populations for present-day Europeans. Nature, 2014, 513, 409-413.	27.8	1,179
3	Genome-wide patterns of selection in 230 ancient Eurasians. Nature, 2015, 528, 499-503.	27.8	1,160
4	Ancient DNA: Do It Right or Not at All. Science, 2000, 289, 1139-1139.	12.6	983
5	Time Dependency of Molecular Rate Estimates and Systematic Overestimation of Recent Divergence Times. Molecular Biology and Evolution, 2005, 22, 1561-1568.	8.9	933
6	Worldwide Phylogeography of Wild Boar Reveals Multiple Centers of Pig Domestication. Science, 2005, 307, 1618-1621.	12.6	729
7	Contamination in Low Microbial Biomass Microbiome Studies: Issues and Recommendations. Trends in Microbiology, 2019, 27, 105-117.	7.7	652
8	Review Paper. Ancient DNA. Proceedings of the Royal Society B: Biological Sciences, 2005, 272, 3-16.	2.6	610
9	Rise and Fall of the Beringian Steppe Bison. Science, 2004, 306, 1561-1565.	12.6	601
10	Species-specific responses of Late Quaternary megafauna to climate and humans. Nature, 2011, 479, 359-364.	27.8	586
11	Diverse Plant and Animal Genetic Records from Holocene and Pleistocene Sediments. Science, 2003, 300, 791-795.	12.6	571
12	Fifty thousand years of Arctic vegetation and megafaunal diet. Nature, 2014, 506, 47-51.	27.8	505
13	Sequencing ancient calcified dental plaque shows changes in oral microbiota with dietary shifts of the Neolithic and Industrial revolutions. Nature Genetics, 2013, 45, 450-455.	21.4	500
14	Time-dependent rates of molecular evolution. Molecular Ecology, 2011, 20, 3087-3101.	3.9	473
15	Mass Survival of Birds Across the Cretaceous-Tertiary Boundary: Molecular Evidence. Science, 1997, 275, 1109-1113.	12.6	470
16	Ancient DNA, pig domestication, and the spread of the Neolithic into Europe. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 15276-15281.	7.1	414
17	Neanderthal behaviour, diet, and disease inferred from ancient DNA in dental calculus. Nature, 2017, 544, 357-361.	27.8	398
18	The Dawn of Human Matrilineal Diversity. American Journal of Human Genetics, 2008, 82, 1130-1140.	6.2	392

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19	Dynamics of Pleistocene Population Extinctions in Beringian Brown Bears. Science, 2002, 295, 2267-2270.	12.6	371
20	Complete mitochondrial genome sequences of two extinct moas clarify ratite evolution. Nature, 2001, 409, 704-707.	27.8	369
21	Ancient DNA from European Early Neolithic Farmers Reveals Their Near Eastern Affinities. PLoS Biology, 2010, 8, e1000536.	5.6	339
22	Ancient mitochondrial DNA provides high-resolution time scale of the peopling of the Americas. Science Advances, 2016, 2, e1501385.	10.3	306
23	Parallel palaeogenomic transects reveal complex genetic history of early European farmers. Nature, 2017, 551, 368-372.	27.8	306
24	A Gondwanan origin of passerine birds supported by DNA sequences of the endemic New Zealand wrens. Proceedings of the Royal Society B: Biological Sciences, 2002, 269, 235-241.	2.6	305
25	Population genetics of Ice Age brown bears. Proceedings of the National Academy of Sciences of the United States of America, 2000, 97, 1651-1654.	7.1	294
26	Ancient DNA Reveals Key Stages in the Formation of Central European Mitochondrial Genetic Diversity. Science, 2013, 342, 257-261.	12.6	293
27	Early Allelic Selection in Maize as Revealed by Ancient DNA. Science, 2003, 302, 1206-1208.	12.6	287
28	Phylogeny and ancient DNA of Sus provides insights into neolithic expansion in Island Southeast Asia and Oceania. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 4834-4839.	7.1	286
29	The Influence of Rate Heterogeneity among Sites on the Time Dependence of Molecular Rates. Molecular Biology and Evolution, 2012, 29, 3345-3358.	8.9	275
30	Abrupt warming events drove Late Pleistocene Holarctic megafaunal turnover. Science, 2015, 349, 602-606.	12.6	274
31	Mitochondrial genomes reveal an explosive radiation of extinct and extant bears near the Miocene-Pliocene boundary. BMC Evolutionary Biology, 2008, 8, 220.	3.2	261
32	Environmental metabarcodes for insects: <i>in silico</i> <scp>PCR</scp> reveals potential for taxonomic bias. Molecular Ecology Resources, 2014, 14, 1160-1170.	4.8	261
33	Reconstructing the Deep Population History of Central and South America. Cell, 2018, 175, 1185-1197.e22.	28.9	259
34	Evidence for Time Dependency of Molecular Rate Estimates. Systematic Biology, 2007, 56, 515-522.	5.6	257
35	Ancient DNA reveals late survival of mammoth and horse in interior Alaska. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 22352-22357.	7.1	255
36	Multiple Geographic Origins of Commensalism and Complex Dispersal History of Black Rats. PLoS ONE, 2011, 6, e26357.	2.5	250

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37	Ancient DNA reveals elephant birds and kiwi are sister taxa and clarifies ratite bird evolution. Science, 2014, 344, 898-900.	12.6	247
38	Conserved sequence motifs, alignment, and secondary structure for the third domain of animal 12S rRNA. Molecular Biology and Evolution, 1996, 13, 150-169.	8.9	239
39	Comparison of environmental DNA metabarcoding and conventional fish survey methods in a river system. Biological Conservation, 2016, 197, 131-138.	4.1	228
40	Novel high-resolution characterization of ancient DNA reveals C > U-type base modification events as the sole cause of post mortem miscoding lesions. Nucleic Acids Research, 2007, 35, 5717-5728.	14.5	219
41	Characterization of Genetic Miscoding Lesions Caused by Postmortem Damage. American Journal of Human Genetics, 2003, 72, 48-61.	6.2	217
42	Independent origins of New Zealand moas and kiwis Proceedings of the National Academy of Sciences of the United States of America, 1992, 89, 8741-8744.	7.1	216
43	Distribution Patterns of Postmortem Damage in Human Mitochondrial DNA. American Journal of Human Genetics, 2003, 72, 32-47.	6.2	210
44	Resolving the evolution of extant and extinct ruminants with high-throughput phylogenomics. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 18644-18649.	7.1	196
45	Aboriginal mitogenomes reveal 50,000 years of regionalism in Australia. Nature, 2017, 544, 180-184.	27.8	195
46	Long-term persistence of bacterial DNA. Current Biology, 2004, 14, R9-R10.	3.9	189
47			
	Molecular Phylogeny, Biogeography, and Habitat Preference Evolution of Marsupials. Molecular Biology and Evolution, 2014, 31, 2322-2330.	8.9	189
48	Molecular Phylogeny, Biogeography, and Habitat Preference Evolution of Marsupials. Molecular Biology and Evolution, 2014, 31, 2322-2330.  Evolutionary explosions and the phylogenetic fuse. Trends in Ecology and Evolution, 1998, 13, 151-156.	8.9	189
48	Biology and Évolutión, 2014, 31, 2322-2330.		
	Biology and Évolution, 2014, 31, 2322-2330.  Evolutionary explosions and the phylogenetic fuse. Trends in Ecology and Evolution, 1998, 13, 151-156.	8.7	188
49	Biology and Évolution, 2014, 31, 2322-2330.  Evolutionary explosions and the phylogenetic fuse. Trends in Ecology and Evolution, 1998, 13, 151-156.  Not just old but old and cold?. Nature, 2001, 410, 771-772.  When did <i>Homo sapiens </i> <ir> /i&gt; first reach Southeast Asia and Sahul?. Proceedings of the National</ir>	8.7 27.8	188
49 50	Biology and Évolution, 2014, 31, 2322-2330.  Evolutionary explosions and the phylogenetic fuse. Trends in Ecology and Evolution, 1998, 13, 151-156.  Not just old but old and cold?. Nature, 2001, 410, 771-772.  When did <i>Homo sapiens </i> first reach Southeast Asia and Sahul?. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 8482-8490.  Survival and recovery of DNA from ancient teeth and bones. Journal of Archaeological Science, 2011,	8.7 27.8 7.1	188 186
49 50 51	Evolutionary explosions and the phylogenetic fuse. Trends in Ecology and Evolution, 1998, 13, 151-156.  Not just old but old and cold?. Nature, 2001, 410, 771-772.  When did <i>Homo sapiens </i> first reach Southeast Asia and Sahul?. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 8482-8490.  Survival and recovery of DNA from ancient teeth and bones. Journal of Archaeological Science, 2011, 38, 956-964.  Neolithic mitochondrial haplogroup H genomes and the genetic origins of Europeans. Nature	8.7 27.8 7.1	188 186 186

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55	Laboratory contamination over time during lowâ€biomass sample analysis. Molecular Ecology Resources, 2019, 19, 982-996.	4.8	161
56	The Oligocene bottleneck and New Zealand biota: genetic record of a past environmental crisis. Proceedings of the Royal Society B: Biological Sciences, 1995, 261, 293-302.	2.6	154
57	Extreme reversed sexual size dimorphism in the extinct New Zealand moa Dinornis. Nature, 2003, 425, 172-175.	27.8	151
58	The evolutionary history of the extinct ratite moa and New Zealand Neogene paleogeography. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 20646-20651.	7.1	150
59	Parallel Evolution of Genes and Languages in the Caucasus Region. Molecular Biology and Evolution, 2011, 28, 2905-2920.	8.9	149
60	Iron Age and Anglo-Saxon genomes from East England reveal British migration history. Nature Communications, 2016, 7, 10408.	12.8	144
61	Flight of the Dodo. Science, 2002, 295, 1683-1683.	12.6	143
62	Ancient mitochondrial DNA from hair. Current Biology, 2004, 14, R463-R464.	3.9	143
63	Late-Quaternary biogeographic scenarios for the brown bear (Ursus arctos), a wild mammal model species. Quaternary Science Reviews, 2011, 30, 418-430.	3.0	143
64	Evolution, Systematics, and Phylogeography of Pleistocene Horses in the New World: A Molecular Perspective. PLoS Biology, 2005, 3, e241.	5.6	142
65	Phylogeography of lions ( <i>Panthera leo </i> ssp.) reveals three distinct taxa and a late Pleistocene reduction in genetic diversity. Molecular Ecology, 2009, 18, 1668-1677.	3.9	142
66	Revising the recent evolutionary history of equids using ancient DNA. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 21754-21759.	7.1	136
67	Testing the Cambrian explosion hypothesis by using a molecular dating technique. Proceedings of the National Academy of Sciences of the United States of America, 1998, 95, 12386-12389.	7.1	135
68	The Genetic Origins of the Andaman Islanders. American Journal of Human Genetics, 2003, 72, 178-184.	6.2	133
69	A molecular analysis of dietary diversity for three archaic Native Americans. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 4317-4322.	7.1	132
70	Four New Avian Mitochondrial Genomes Help Get to Basic Evolutionary Questions in the Late Cretaceous. Molecular Biology and Evolution, 2004, 21, 974-983.	8.9	131
71	Using ancient DNA to study the origins and dispersal of ancestral Polynesian chickens across the Pacific. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 4826-4831.	7.1	131
72	Identifying Genetic Traces of Historical Expansions: Phoenician Footprints in the Mediterranean. American Journal of Human Genetics, 2008, 83, 633-642.	6.2	127

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73	From the field to the laboratory: Controlling DNA contamination in human ancient DNA research in the high-throughput sequencing era. Science and Technology of Archaeological Research, 2017, 3, 1-14.	2.4	126
74	Molecular phylogeny of coleoid cephalopods (Mollusca: Cephalopoda) using a multigene approach; the effect of data partitioning on resolving phylogenies in a Bayesian framework. Molecular Phylogenetics and Evolution, 2005, 37, 426-441.	2.7	125
<b>7</b> 5	Mitochondrial Phylogenomics of Modern and Ancient Equids. PLoS ONE, 2013, 8, e55950.	2.5	123
76	Using palaeoenvironmental DNA to reconstruct past environments: progress and prospects. Journal of Quaternary Science, 2014, 29, 610-626.	2.1	116
77	Ancient DNA analysis of dental calculus. Journal of Human Evolution, 2015, 79, 119-124.	2.6	114
78	DNA from Museum Specimens. , 1994, , 149-165.		109
79	Climate change not to blame for late Quaternary megafauna extinctions in Australia. Nature Communications, 2016, 7, 10511.	12.8	109
80	Y-Chromosomal Diversity in Lebanon Is Structured by Recent Historical Events. American Journal of Human Genetics, 2008, 82, 873-882.	6.2	106
81	Evolution of the extinct Sabretooths and the American cheetah-like cat. Current Biology, 2005, 15, R589-R590.	3.9	105
82	Synergistic roles of climate warming and human occupation in Patagonian megafaunal extinctions during the Last Deglaciation. Science Advances, 2016, 2, e1501682.	10.3	102
83	DNA capture and next-generation sequencing can recover whole mitochondrial genomes from highly degraded samples for human identification. Investigative Genetics, 2013, 4, 26.	3.3	101
84	The Genographic Project Public Participation Mitochondrial DNA Database. PLoS Genetics, 2007, 3, e104.	3.5	99
85	A mitochondrial revelation of early human migrations to the Tibetan Plateau before and after the last glacial maximum. American Journal of Physical Anthropology, 2010, 143, 555-569.	2.1	98
86	Indo-European and Asian origins for Chilean and Pacific chickens revealed by mtDNA. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 10308-10313.	7.1	95
87	Full of Sound and Fury: History of Ancient DNA. Annual Review of Ecology, Evolution, and Systematics, 1999, 30, 457-477.	6.7	94
88	Coprolite deposits reveal the diet and ecology of the extinct New Zealand megaherbivore moa (Aves,) Tj ETQq(	0 0 0 <sub>3</sub> ;gBT /0	Overlock 10 Ti
89	Relict or colonizer? Extinction and range expansion of penguins in southern New Zealand. Proceedings of the Royal Society B: Biological Sciences, 2009, 276, 815-821.	2.6	94
90	The origin, current diversity and future conservation of the modern lion (Panthera leo). Proceedings of the Royal Society B: Biological Sciences, 2006, 273, 2119-2125.	2.6	90

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91	Ancient DNA from marine sediments: Precautions and considerations for seafloor coring, sample handling and data generation. Earth-Science Reviews, 2019, 196, 102887.	9.1	90
92	Using Ancient DNA to Understand Evolutionary and Ecological Processes. Annual Review of Ecology, Evolution, and Systematics, 2014, 45, 573-598.	8.3	88
93	The skin microbiome: Associations between altered microbial communities and disease. Australasian Journal of Dermatology, 2015, 56, 268-274.	0.7	88
94	Substitutions in woolly mammoth hemoglobin confer biochemical properties adaptive for cold tolerance. Nature Genetics, 2010, 42, 536-540.	21.4	86
95	Did the Denisovans Cross Wallace's Line?. Science, 2013, 342, 321-323.	12.6	85
96	Divergence time estimates for major cephalopod groups: evidence from multiple genes. Cladistics, 2006, 22, 89-96.	3.3	82
97	Relationships of the extinct moa-nalos, flightless Hawaiian waterfowl, based on ancient DNA. Proceedings of the Royal Society B: Biological Sciences, 1999, 266, 2187-2193.	2.6	81
98	Early cave art and ancient DNA record the origin of European bison. Nature Communications, 2016, 7, 13158.	12.8	81
99	High-Resolution Analysis of Cytosine Methylation in Ancient DNA. PLoS ONE, 2012, 7, e30226.	2.5	80
100	Ancient DNA and island endemics. Nature, 1996, 381, 484-484.	27.8	78
101	Ancient DNA Reveals Prehistoric Gene-Flow from Siberia in the Complex Human Population History of North East Europe. PLoS Genetics, 2013, 9, e1003296.	3.5	78
102	Genome of the Tasmanian tiger provides insights into the evolution and demography of an extinct marsupial carnivore. Nature Ecology and Evolution, 2018, 2, 182-192.	7.8	78
103	Ancient DNA Provides New Insights into the Evolutionary History of New Zealand's Extinct Giant Eagle. PLoS Biology, 2005, 3, e9.	5.6	77
104	Evolution of the mane and group-living in the lion (Panthera leo): a review. Journal of Zoology, 2004, 263, 329-342.	1.7	76
105	Human Migration through Bottlenecks from Southeast Asia into East Asia during Last Glacial Maximum Revealed by Y Chromosomes. PLoS ONE, 2011, 6, e24282.	2.5	75
106	An updated tree of Y-chromosome Haplogroup O and revised phylogenetic positions of mutations P164 and PK4. European Journal of Human Genetics, 2011, 19, 1013-1015.	2.8	74
107	Limitations and recommendations for successful DNA extraction from forensic soil samples: A review. Science and Justice - Journal of the Forensic Science Society, 2014, 54, 238-244.	2.1	74
108	Sequence preservation of osteocalcin protein and mitochondrial DNA in bison bones older than 55 ka. Geology, 2002, 30, 1099.	4.4	73

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109	High-Resolution Coproecology: Using Coprolites to Reconstruct the Habits and Habitats of New Zealand's Extinct Upland Moa (Megalapteryx didinus). PLoS ONE, 2012, 7, e40025.	2.5	73
110	Discovery of lost diversity of paternal horse lineages using ancient DNA. Nature Communications, 2011, 2, 450.	12.8	72
111	A Megafauna's Microfauna: Gastrointestinal Parasites of New Zealand's Extinct Moa (Aves:) Tj ETQq1 1 0	.784314 r 2.5	gBT/Overlo
112	A Paleogenomic Reconstruction of the Deep Population History of the Andes. Cell, 2020, 181, 1131-1145.e21.	28.9	69
113	Experimental conditions improving inâ€solution target enrichment for ancient <scp>DNA</scp> . Molecular Ecology Resources, 2017, 17, 508-522.	4.8	67
114	Antarctic eukaryotic soil diversity of the Prince Charles Mountains revealed by high-throughput sequencing. Soil Biology and Biochemistry, 2016, 95, 112-121.	8.8	66
115	Ancient mitochondrial DNA reveals convergent evolution of giant short-faced bears (Tremarctinae) in North and South America. Biology Letters, 2016, 12, 20160062.	2.3	65
116	Using Amplicon Sequencing To Characterize and Monitor Bacterial Diversity in Drinking Water Distribution Systems. Applied and Environmental Microbiology, 2015, 81, 6463-6473.	3.1	63
117	Connecting the Greenland ice-core and Uâ^•Th timescales via cosmogenic radionuclides: testing the synchroneity of Dansgaard–Oeschger events. Climate of the Past, 2018, 14, 1755-1781.	3.4	62
118	A global environmental crisis 42,000 years ago. Science, 2021, 371, 811-818.	12.6	61
119	Resistance of degraded hair shafts to contaminant DNA. Forensic Science International, 2006, 156, 208-212.	2.2	60
120	Ancient <scp>DNA</scp> identifies postâ€glacial recolonisation, not recent bottlenecks, as the primary driver of contemporary mt <scp>DNA</scp> phylogeography and diversity in Scandinavian brown bears. Diversity and Distributions, 2013, 19, 245-256.	4.1	59
121	Robust estimates of extinction time in the geological record. Quaternary Science Reviews, 2012, 33, 14-19.	3.0	58
122	The Basque Paradigm: Genetic Evidence of a Maternal Continuity in the Franco-Cantabrian Region since Pre-Neolithic Times. American Journal of Human Genetics, 2012, 90, 486-493.	6.2	58
123	Resolving lost herbivore community structure using coprolites of four sympatric moa species (Aves:) Tj ETQq1 1 (2013, 110, 16910-16915.	0.784314 7.1	rgBT /Overlo 57
124	Human Origins and Ancient Human DNA. Science, 2001, 292, 1655-1656.	12.6	56
125	An optimized method for the extraction of ancient eukaryote DNA from marine sediments. Molecular Ecology Resources, 2020, 20, 906-919.	4.8	55
126	Pinghua population as an exception of Han Chinese's coherent genetic structure. Journal of Human Genetics, 2008, 53, 303-313.	2.3	54

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127	Coprolites reveal ecological interactions lost with the extinction of New Zealand birds. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 1546-1551.	7.1	54
128	Ancient plant DNA in the genomic era. Nature Plants, 2018, 4, 394-396.	9.3	54
129	Lost populations and preserving genetic diversity in the lion Panthera leo: Implications for its ex situ conservation. Conservation Genetics, 2006, 7, 507-514.	1.5	53
130	Palaeogeography and voyage modeling indicates early human colonization of Australia was likely from Timor-Roti. Quaternary Science Reviews, 2018, 191, 431-439.	3.0	52
131	Evolution of the moa and their effect on the New Zealand flora. Trends in Ecology and Evolution, 1993, 8, 433-437.	8.7	51
132	Geographical Structure of the Yâ€chromosomal Genetic Landscape of the Levant: A coastalâ€inland contrast. Annals of Human Genetics, 2009, 73, 568-581.	0.8	51
133	Forensic soil DNA analysis using high-throughput sequencing: A comparison of four molecular markers. Forensic Science International: Genetics, 2014, 13, 176-184.	3.1	51
134	Evolution and extinction of the giant rhinoceros Elasmotherium sibiricum sheds light on late Quaternary megafaunal extinctions. Nature Ecology and Evolution, 2019, 3, 31-38.	7.8	50
135	Early Last Interglacial ocean warming drove substantial ice mass loss from Antarctica. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 3996-4006.	7.1	50
136	Y-Chromosome and mtDNA Genetics Reveal Significant Contrasts in Affinities of Modern Middle Eastern Populations with European and African Populations. PLoS ONE, 2013, 8, e54616.	2.5	49
137	Ancient mitochondrial genome reveals unsuspected taxonomic affinity of the extinct Chatham duck (Pachyanas chathamica) and resolves divergence times for New Zealand and sub-Antarctic brown teals. Molecular Phylogenetics and Evolution, 2014, 70, 420-428.	2.7	49
138	Ancient and modern genomes unravel the evolutionary history of the rhinoceros family. Cell, 2021, 184, 4874-4885.e16.	28.9	49
139	Afghanistan's Ethnic Groups Share a Y-Chromosomal Heritage Structured by Historical Events. PLoS ONE, 2012, 7, e34288.	2.5	46
140	Sporormiella as a proxy for non-mammalian herbivores in island ecosystems. Quaternary Science Reviews, 2011, 30, 915-920.	3.0	44
141	The effect of climate and environmental change on the megafaunal moa of New Zealand in the absence of humans. Quaternary Science Reviews, 2012, 50, 141-153.	3.0	44
142	Rapid megafaunal extinction following human arrival throughout the New World. Quaternary International, 2013, 308-309, 273-277.	1.5	44
143	Broadening the taxonomic scope of coral reef palaeoecological studies using ancient DNA. Molecular Ecology, 2019, 28, 2636-2652.	3.9	44
144	Phylogeny and Evolution of 12S rDNA in Gruiformes (Aves). , 1997, , 121-158.		43

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145	New Zealand Passerines Help Clarify the Diversification of Major Songbird Lineages during the Oligocene. Genome Biology and Evolution, 2015, 7, 2983-2995.	2.5	43
146	Review of Toxic Epidermal Necrolysis. International Journal of Molecular Sciences, 2016, 17, 2135.	4.1	43
147	Ancient <scp>DNA</scp> from the extinct South American giant glyptodont <i>Doedicurus</i> sp. (Xenarthra: Glyptodontidae) reveals that glyptodonts evolved from Eocene armadillos. Molecular Ecology, 2016, 25, 3499-3508.	3.9	43
148	Dire wolves were the last of an ancient New World canid lineage. Nature, 2021, 591, 87-91.	27.8	43
149	Ancient DNA Clarifies the Evolutionary History of American Late Pleistocene Equids. Journal of Molecular Evolution, 2008, 66, 533-538.	1.8	42
150	DNA content and distribution in ancient feathers and potential to reconstruct the plumage of extinct avian taxa. Proceedings of the Royal Society B: Biological Sciences, 2009, 276, 3395-3402.	2.6	41
151	Integrating multiple lines of evidence into historical biogeography hypothesis testing: a <i>Bison bison</i> case study. Proceedings of the Royal Society B: Biological Sciences, 2014, 281, 20132782.	2.6	41
152	Closing the gap: New data on the last documented <i>Myotragus</i> and the first human evidence on Mallorca (Balearic Islands, Western Mediterranean Sea). Holocene, 2016, 26, 1887-1891.	1.7	41
153	Toxic Epidermal Necrolysis and Steven–Johnson Syndrome: A Comprehensive Review. Advances in Wound Care, 2020, 9, 426-439.	5.1	41
154	A Re-Appraisal of the Early Andean Human Remains from Lauricocha in Peru. PLoS ONE, 2015, 10, e0127141.	2.5	41
155	Long-term survival of ancient DNA in Egypt: Response to Zink and Nerlich (2003). American Journal of Physical Anthropology, 2005, 128, 110-114.	2.1	40
156	Influences of history, geography, and religion on genetic structure: the Maronites in Lebanon. European Journal of Human Genetics, 2011, 19, 334-340.	2.8	40
157	Historical stocking data and 19th century <scp>DNA</scp> reveal humanâ€induced changes to native diversity and distribution of cutthroat trout. Molecular Ecology, 2012, 21, 5194-5207.	3.9	40
158	The origins of the enigmatic Falkland Islands wolf. Nature Communications, 2013, 4, 1552.	12.8	40
159	Modern management of acne. Medical Journal of Australia, 2017, 206, 41-45.	1.7	40
160	Population Differentiation of Southern Indian Male Lineages Correlates with Agricultural Expansions Predating the Caste System. PLoS ONE, 2012, 7, e50269.	2.5	40
161	The Complete Mitochondrial Genome of an 11,450-year-old Aurochsen (Bos primigenius) from Central Italy. BMC Evolutionary Biology, 2011, 11, 32.	3.2	39
162	A new subhaplogroup of native American Y-Chromosomes from the Andes. American Journal of Physical Anthropology, 2011, 146, 553-559.	2.1	38

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163	Evidence of Pre-Roman Tribal Genetic Structure in Basques from Uniparentally Inherited Markers. Molecular Biology and Evolution, 2012, 29, 2211-2222.	8.9	37
164	Clan, language, and migration history has shaped genetic diversity in Haida and Tlingit populations from Southeast Alaska. American Journal of Physical Anthropology, 2012, 148, 422-435.	2.1	37
165	Uncertainties in dating constrain model choice for inferring extinction time from fossil records. Quaternary Science Reviews, 2015, 112, 128-137.	3.0	37
166	DNA adsorption by nanocrystalline allophane spherules and nanoaggregates, and implications for carbon sequestration in Andisols. Applied Clay Science, 2016, 120, 40-50.	5.2	37
167	Widespread male sex bias in mammal fossil and museum collections. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 19019-19024.	7.1	37
168	Reply to Storey $\langle i \rangle$ et al. $\langle i \rangle$ : More DNA and dating studies needed for ancient El Arenal-1 chickens. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, .	7.1	36
169	A Lost Link between a Flightless Parrot and a Parasitic Plant and the Potential Role of Coprolites in Conservation Paleobiology. Conservation Biology, 2012, 26, 1091-1099.	4.7	36
170	Predicting the origin of soil evidence: High throughput eukaryote sequencing and MIR spectroscopy applied to a crime scene scenario. Forensic Science International, 2015, 251, 22-31.	2.2	36
171	Comment on "Whole-genome analyses resolve early branches in the tree of life of modern birds― Science, 2015, 349, 1460-1460.	12.6	36
172	Using environmental (e)DNA sequencing for aquatic biodiversity surveys: a beginner's guide. Marine and Freshwater Research, 2017, 68, 20.	1.3	36
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